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Fremgangsmåde til identifikation af biologisk aktive peptider og nucleinsyrer

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A METHOD FOR IDENTIFICATION OF BIOLOGICALLY ACTIVE PEPTIDES AND NUCLEIC ACIDS

This invention concerns a novel method for identification of new peptides and post-translationally modified peptides with biological activity.

BACKGROUND OF THE INVENTION

During the last five years the technology for expressing, testing and identifying millions of different random peptide sequences has evolved dramatically. Such peptide libraries can be used for identification of new biologically active peptides, and therefore the technology has added an exciting and very promising new epoch to the field of drug development.

The known peptide library techniques can at present be divided into two fundamentally different groups: The random synthetic peptide libraries, in which the random peptides are produced chemically, and the random biosynthetic peptide libraries, in which the random peptides are encoded by partly or totally random DNA sequences and subsequently synthesized by ribosomes.

The synthetic peptide libraries.

Synthetic peptide libraries containing millions of peptides can be produced by combinatorial peptide chemistry and may either be synthesized in soluble form (R.A. Houghten et al. Nature, 354, 84-86, 1991) or remain immobilized on the peptide resin beads (A. Furka et al., Int. J. Peptide Protein Res. 37, 487-493, 1991; K. S. Lam et al., Nature, 354, 82-84, 1991). Using either of these approaches different receptor ligands have been isolated.

The advantage of the soluble peptide libraries compared to solid phase immobilized peptide libraries is that soluble peptides may bind more sterically unhindered to the receptors in question. In the synthetic peptide library technique proposed by Furka et al. 1991 and Lam et al. 1991, respectively, the most important improvement, on the other hand, was the approach of having only one type of peptide sequence on each bead ("One bead - one peptide"). This enables direct selection and eventually sequencing of the putative active peptide ligand on a single bead using e.g. Edman degradation. Using this technology active peptides including peptides consisting of D-amino acids or other unnatural amino acids can be identified (B. Gissel et al. J. Peptide Science. In Press, 1995).

The biosynthetic peptide libraries.

Bacteriophage expression vectors have been constructed that can display peptides on the phage surface (S.E. Cwirla et al, Proc. Natl. Acad. Sci. USA, 87, 6378-6382, 1990). Each peptide is encoded by a randomly mutated region of the phage genome, so sequencing of the relevant DNA region from the bacteriophage found to bind a receptor will reveal the amino acid sequence of the peptide ligand. A phage containing a peptide ligand is detected by repeated panning procedures which enrich the phage population for a strong receptor binding phage (J.K. Scott, TIBS, 17, 241-245, 1992).

Bacteria have also been used for expression of similar peptide libraries. The peptides can be fused to an exported protein, such as an antibody, which can be immobilized on a solid support. By screening the solid support with an appropriate soluble receptor the bacterial clone producing the putative peptide ligand can be identified (M.G. Cull et al, Proc. Natl. Acad. Sci. USA, 89, 1865-1869, 1992).

Another described method for preparing large pools of different possibly active compounds is by the use of libraries consisting of randomized ribonucleotides or deoxyribonucleotides, the so-called aptamer libraries. The aptamers are generated in E. coli from a plasmid vector containing randomized DNA. From these libraries structures

with biological activity have been identified (L.C. Bock et al, Nature, 355, 564-566, 1992).

PURPOSE OF THE INVENTION

In order to use the prior art methods for identifying biologically active peptides and nucleic acids, it is necessary to possess a detailed knowledge about the molecular mechanisms involved in a certain biological process. If these mechanisms are known, it may subsequently be possible to develop antagonists or agonists of the receptors, enzymes, etc. involved using said methods. The problem to be solved by the present invention is i.a. to overcome the need for said detailed knowledge.

SUMMARY OF THE INVENTION

According to the present invention the peptides or the ribonucleic acids are identified from biosynthetically expressed eukaryotic libraries containing millions of partly or totally random peptides and ribonucleic acids. The peptides and ribonucleic acids are synthesized by the cells from random DNA sequences which have been effectively transduced into the cells. Some of the peptides or ribonucleic acids in the library will affect important biological functions in the cells which express them. Cells which change phenotype due to the presence of such substances can be isolated, and their chemical structure can subsequently be clarified by sequencing of the DNA which encodes them. Such peptides could possibly be used therapeutically or as lead compounds for future drug development.

Accordingly, the method of the invention comprises the following steps: (a) production of a pool of appropriate vectors each containing totally or partly random DNA sequences, (b) efficient transduction of said vectors into a number of identical, e.g. mammalian, cells in such a way that a single ribonucleic acid and possibly peptide is expressed or a limited number of different random ribonucleic acids and peptides are expressed by each cell, (c) screening of said transduced cells to see whether some of them have changed a certain phenotypic trait, (d) selection and cloning of said changed

cells, (e) isolation and sequencing of the vector DNA in said phenotypically changed cells, and (f) deducing the RNA and peptide sequences from the DNA sequence.

In connection with this invention the term "peptide" shall be understood to comprise also a peptide sequence introduced into or fused to a larger protein.

BRIEF DESCRIPTION OF THE DRAWING

Figure 1 is a schematic drawing of a standard retroviral peptide expression vector. The plasmid form of the vector (top) carries a cytomegalovirus (CMV) promoter directing expression of a retroviral RNA (middle) with a backbone (R, U5, PBS, Ψ, PPT, U3, and R) from Akv murine leukaemia virus and a zeomycin resistance gene (Zeo) followed by an internal ribosomal entry site (IRES) from EMC virus directing peptide translation. The vector provirus in the target cell (below) contains a regenerated retroviral long terminal repeat - LTR (U3, R, and U5). The CMV promoter sequence provides a unique tag for efficient initial PCR mutagenesis and amplification. The size of the vector without an inserted peptide expression cassette is 2.6 kb.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

A built-in requirement of all the presently known peptide library techniques is the necessity of a detailed knowledge about the mechanisms by which a given receptor or enzyme regulates a certain phenotypic trait of the cell. This receptor or enzyme furthermore has to be available in a relatively pure form before a ligand can be selected in either of the two types of peptide libraries. When potential peptide ligands eventually have been identified, functional assays have to be performed to determine whether the ligands exert antagonistic or agonistic effects on the desired cellular phenotypic trait.

The method according to the present invention overcomes this major problem. By the present method it is thus not necessary to know the chain of mechanisms, receptors, signalling pathways, enzymes etc. which generate the phenomenon inside or on the

surface of the cell since it is the resulting biological effect or phenotypic trait which is screened for. This is achieved by the following steps: (a) production of a pool of appropriate vectors each containing totally or partly random DNA sequences, (b) efficient transduction of said vectors into a number of identical eukaryotic, e.g. mammalian, cells in such a way that only a single ribonucleic acid and peptide species is expressed ("one cell - one peptide or ribonucleic acid") or optionally a limited number of different random ribonucleic acids and peptides are expressed by each cell, (c) screening of said transduced cells to see whether some of these have changed a certain phenotypic trait, (d) selection and cloning of said changed cells, (e) isolation and sequencing of the vector DNA in said phenotypically changed cells, and (f) deducing the RNA and peptide sequences from the DNA sequence. Either the RNA or the peptide encoded by the isolated DNA sequences may be the cause of said phenotypic changes of the cell and may therefore possess biological activity.

The introduced peptides are expressed e.g. in the cytoplasm of biologically interesting cells, which before that were totally identical, using e.g. the retroviral vector systems described in Example 1. They are expressed from a pool of vectors containing random DNA sequences which has been constructed e.g. as described in Example 1. Using an appropriate ratio between infective retrovirus and non-infected cells only a single DNA copy derived from the pool of retrovirus vectors is introduced into each cell. The major advantage by this "One cell - one peptide or ribo-oligonucleotide" concept is that cells which have changed phenotypically upon the introduction of peptides can be isolated by cloning and selection methods, and that the active peptide causing the phenotypic change can subsequently be identified. This is accomplished by isolating the DNA fragment encoding the peptide, e.g. by Polymerase Chain Reaction (PCR) technology, and subsequently identifying the DNA sequence.

During the initial screening procedure a larger number of retrovirus vectors can be introduced into each cell which enables the individual cell to express a number of different peptides or RNA molecules. When a phenotypically changed cell clone subsequently has been isolated all retroviral DNA in that particular clone can be isolated by PCR, and the PCR product can be used for re-transfection of the

packaging cells ordinarily used for virus production. The retroviral vectors isolated from these packaging cells can subsequently be used for transduction of new biologically interesting cells using the "one cell - one peptide or ribonucleic acid" concept. Finally, after a second cloning procedure the active substance can be identified as described above.

The cells which are found to have changed phenotypically upon the introduction of the random DNA sequences could alternatively have changed as a consequence of interactions with the RNA molecule transcribed from the introduced DNA, in analogy to the described libraries consisting of randomized ribonucleotides or deoxyribonucleotides, the so-called aptamer libraries. Such RNA molecules would therefore also possess biological activity. Furthermore, the observed effect could also be due to biological activity of carbohydrate moieties or other post-translational modifications on the expressed peptides in the cell. Using an appropriate purification-tag on the peptides in the library, it would be possible in that case to purify these and analyze the exact chemical structure of the post-translational modifications in question.

Since the efficiency of the non-viral methods commonly used for stable gene transfer into mammalian cells is very low, it would not be possible to establish a peptide expression library in mammalian cells by such methods. In addition non-viral methods generally lead to multiple integrations of DNA in the cell genome in disagreement with the "one cell one peptide concept". In order to achieve the necessary high efficiency single gene copy transfer a viral vector must be used. Very recently cDNA expression libraries which were constructed using retroviral vectors have been described. From such libraries cytokines and cellular growth factors have been isolated (A.J.M. Murphy et al., Proc. Natl. Acad. Sci. USA, 84, 8277-8281, 1987., B.Y. Wong et al., J. Virol., 68, 5523-31, 1994., J.R. Rayner et al., Mol. Cell. Biol., 14, 880-887, 1994). Expression of well defined peptides in transfected eukaryotic cells has also previously been established, although not using retroviral vectors (M.S. Malnati et al., Nature, 357, 702-704, 1992., E.O. Long et al., J. Immunol., 153, 1487-1494, 1994). A library of random peptides has never been expressed in mammalian cells with the purpose of identifying biologically active peptides or ribonucleic acids.

Immunology is an important biological field where the method according to the invention can be used. T cells only recognize fragments of protein antigens, and only if these are bound to MHC molecules. Two types of MHC molecules - the class I and II molecules - present antigen fragments to T cells. The peptides presented by MHC class I molecules, which are on the surface of essentially all nucleated cells, are 8-9 amino acids long and generally derived from proteins in the cytosol of the cell. These can be self-proteins, viral proteins, peptides introduced into the cytosol by transfection or tumor antigens. It is of considerable interest to be able to identify such peptides or T cell epitopes e.g. with regard to vaccine development or in immunotherapy of cancer. Identification of such fragments is, however, a very difficult, demanding and some times impossible task requiring large amounts of affinity purified MHC molecules derived from the tumor cell in question and iterative combinations of advanced mass spectrometry, HPLC and functional T cell assays. Furthermore, most peptide antigens cannot be identified due to the presence of very low amounts of the individual peptides on the MHC molecules. In Example 2 it is demonstrated that the method according to the present invention can be used for identification of said T cell epitopes.

Cell lines expressing biologically important surface molecules can also be transduced with a random peptide library according to the invention. An example of such molecules could be the B7 co-stimulatory molecule, which is known to be important for activation of T cells, or the selectin family of proteins which are known to be involved in the homing of inflammatory cells to inflamed tissue. Cells which change phenotype (e.g. either up- or down-regulate B7) can be selected and cloned as described in Example 3. After isolation of the transduced DNA by PCR new cells can be transduced with the isolated DNA to confirm the observation. Subsequently, the peptide sequence can be deduced from the DNA sequence.

The invention is illustrated by the following examples:

EXAMPLE 1

Construction of an intracellular eukaryotic peptide library

A retrovirus vector capable of expressing random peptide sequences is constructed. If the random DNA sequences used in the vector were produced using conventional random oligonucleotide synthesis a large number of stop codons inevitably would be introduced. Furthermore, due to the degeneracy of the genetic code an uneven distribution of the encoded amino acids would be the result. We avoid this by producing the random DNA sequences by random codon synthesis: An appropriate amount of resin used for solid phase oligonucleotide synthesis (optionally already containing a DNA sequence corresponding to an appropriate vector cloning site) is divided into 20 different portions. On portion no. 1 a conventional solid phase chemical synthesis of three bases corresponding to a codon encoding the amino acid, alanine, is performed. On portion no. 2 a codon encoding cysteine is synthesized and so forth. When each of the 20 portions have been coupled with codons corresponding to each of the natural amino acids, all portions are mixed and divided again into 20 equally sized resin portions. The codon synthesis is then repeated again, and the whole procedure is repeated until the desired randomized DNA sequence has been synthesized - e.g. corresponding to 6-10 random amino acids. This can also be achieved by using blocked and protected trinucleotide phosphoramidites encoding the 20 natural amino acids in a total random oligonucleotide synthesis (J. Sondek et al., Proc. Natl. Acad. Sci. USA, 89, 3581-5, 1992). Finally, other appropriate vector cloning sites can be synthesized on all the oligonucleotides before they eventually are cleaved from the resin.

The pool of random synthetic oligonucleotides can be used to generate a pool of vectors with random sequences in appropriate positions either by restriction cleavage and ligation or, preferentially, to avoid inefficient ligation steps, by PCR-mutagenesis. The procedures follow the principles of site-directed PCR-mediated mutagenesis (S. Perrin et al., Nucl. Acids Res. 18, 7433-38, 1990), but the methodology has been adapted to deliver a complex mixture of products. Briefly, the random oligonucleotides carrying vector sequences flanking the random sequence are used as primers in a PCR reaction together with a unique terminal vector primer. In order to retain complexity large

quantities of template as well as of vector and randomized primers are used, and product diversity is further ensured by pooling of multiple independent PCR-reactions. Subsequently, an overlapping PCR fragment containing the remaining vector segment is produced by standard PCR. Finally, this overlapping segment is joined with the PCR fragments containing the random DNA using another unique set of terminal primers.

To maintain diversity, the PCR-generated linear vector DNA is used directly for transfection of packaging cells, and virions containing the pool of different vectors are harvested under transient conditions. Small bicistronic single transcript vectors containing a zeomycin (zeo) resistance gene followed by an internal ribosomal entry site (IRES) from EMC virus and the random peptide expression cassette are used. The zeo gene functions as a selection marker to allow titre determination and elimination of non-transduced cells, if necessary. Other available relevant vectors employ neomycin resistance gene instead of zeo or have the peptide expression cassette in front of the EMC internal ribosome entry site and a resistance gene. Alternatively, even smaller vectors, carrying only the peptide expression cassette and lacking a selection marker can also be used.

The use of small vectors (below 3 kb of DNA) has the major advantage of allowing simple PCR-mutagenesis and amplification without ligation and cloning steps. Another important advantage of using small vectors is that the vectors in a pool of target cells can be amplified directly by PCR and retransfected into packaging cells, hence allowing multiple rounds of selection to remove time-consuming analysis of false positives or contaminating cells. Direct sequence analysis of the derived random plasmid clones is used to assure the randomness of the expression library. The standard vector capable of expressing the random peptide library is shown schematically in Fig. 1.

Restrictions upon the "randomness" of the peptide sequence can be introduced, for the purpose of limiting the number of available sequences in the mammalian cellular library and for introduction of e.g. N-glycosylation sites, or other post-translational modifications of all expressed peptides if so desired. Purification tags - e.g. poly-His

or others - can also be included in the expressed peptides for facilitating the purification and identification of the peptide itself. This is necessary for the identification of post-translational modifications, which were not obvious from the peptide sequence.

A population of eukaryotic cells is infected with the retrovirus carrying genetic constructs containing random DNA sequences which encode a library of millions of random peptides. Initially an excess number of virus compared to eukaryotic cells can be used. This leads to expression of a number of different peptides within each eukaryotic cell. These cells can subsequently be screened as described below, and the DNA can be isolated e.g. by PCR and used for reinfection of other cells. If an appropriate ratio between the number of retrovirus containing the random DNA sequences and cells is chosen, each cell will be transduced with a different random DNA sequence ("One cell - one peptide"). This eventually enables the identification of an active peptide.

The peptide may optionally be targeted to different compartments in the cell by incorporating appropriate signal sequences in the translated sequences.

EXAMPLE 2

Identification of T cell epitopes by the use of mammalian intracellular expression libraries

The interleukin 2 (Il-2) dependent cell line, CTLL-2, is transfected with the murine Major Histocompatibility (MHC) class I molecule, K^b. Subsequently this cell line is infected with a retrovirus peptide library which was described in Example 1. This CTLL-2 peptide library expresses a wide range of random peptides, and if appropriate K^b associated anchor residues known to be important for peptide binding to K^b are introduced in the retroviral peptide sequence, a large library of peptides bound to K^b are presented on the surface of the CTLL-2 cells.

K^b restricted T cell hybridomas are generated against an appropriate virus antigen using conventional cellular immunological technology (Current Protocols in Immunology, Eds. Coligan et al., NIH). Such hybridomas secrete Il-2 upon recognition of antigen. A T cell hybridoma, which recognizes an unknown K^b bound virus T cell epitope, is subsequently incubated with samples of the K^b CTLL-2 library. If the hybridoma recognizes a peptide, the CTLL-2 cell presenting the peptide will be stimulated to proliferate by the Il-2 secreted by the hybridoma. In that way the CTLL-2 cell expressing the unknown virus T cell epitope can be selected and cloned. From this clone the DNA sequence encoding the peptide epitope in question can be isolated using PCR technology followed by conventional DNA sequencing. This eventually leads to identification of the unknown virus T cell epitope.

EXAMPLE 3

Identification of biologically active peptides or ribonucleic acids which regulate cell surface expression of proteins

Cells expressing the immunoregulatory membrane molecule, B7, are infected with the random peptide libraries constructed as described in Example 1. In this example a random eight-mer peptide library is introduced.

Using specific monoclonal antibodies the expression of B7 is analyzed by conventional methods. Cells which up- or down-regulate B7 can be selected either positively, e.g. using Fluorescence Activated Cell Sorting, or negatively, e.g. using appropriate antibodies in combination with lysis by complement.

Cells which show changes in expression of B7 are cloned by conventional means, and the DNA introduced by retroviral vectors is isolated using PCR and a set of retrovirus specific primers. The peptide sequence or possibly the RNA corresponding to said DNA may be able to modify the expression of B7 and hence the activation of T cells. This can subsequently be tested in conventional T cell assays.

PATENT CLAIMS

1. A method for identification of biologically active peptides and nucleic acids comprising the following steps: (a) production of a pool of appropriate vectors each containing totally or partly random DNA sequences, (b) efficient transduction of said vectors into a number of identical eukaryotic cells in such a way that a single ribonucleic acid and possibly peptide is expressed or a limited number of different random ribonucleic acids and peptides are expressed by each cell, (c) screening of said transduced cells to see whether some of them have changed a certain phenotypic trait, (d) selection and cloning of said changed cells, (e) isolation and sequencing of the vector DNA in said phenotypically changed cells, and (f) deducing the RNA and peptide sequences from the DNA sequence.

2. A method according to claim 1 in which the amino acid sequences of the random peptide library are encoded by synthetic DNA sequences/oligonucleotides produced by codon split synthesis, where defined DNA codons are synthesized in a random order.

3. A method according to claim 1 in which the amino acid sequences of the random peptide library are encoded by synthetic DNA sequences/oligonucleotides produced by conventional random oligonucleotide synthesis.

4. A method according to any one of claims 1-3 in which the random DNA sequences are introduced into the expression vector by the principle of site directed PCR-mediated mutagenesis hereby ensuring the complexity of the library.

5. A method according to any one of claims 1-4 in which the random DNA sequences are introduced into the number of eukaryotic cells in such a way that only one DNA sequence is introduced in each cell, one cell expressing one ribonucleic acid and possibly one peptide, thus enabling a particular sequence to by isolated and analyzed.

6. A method according to any one of claims 1-5 in which the random DNA sequences are introduced into the eukaryotic cells by the use of appropriate viral vectors selected from e.g. retrovirus or vaccinia virus.

7. A method according to claim 6 in which the random DNA sequences are produced as linear PCR products which are directly introduced into the virus packaging cells by non-viral transfection methods.

8. A method according to claim 6 or 7 in which the viral DNA introduced into the cells is amplified directly by PCR and used for retransfection of new target cells with the purpose of eliminating false positives and/or enabling the "one cell - one ribonucleic acid and peptide" concept.

9. A method according to any one of claims 1-8 in which appropriate restrictions upon the random nature of the expressed peptides are introduced such as e.g. glycosylation sites and anchor residues.

10. A method according to any one of claims 1-9 in which purification tags are encoded by the introduced DNA in such a way that such tags are attached to the expressed peptides.

11. A method according to any one of claims 1-10 in which appropriate signal peptides, other leader molecules or recognition sequences also are encoded by the introduced DNA in such a way that they are fused to the expressed random peptides enabling these to be directed towards defined cellular compartments.

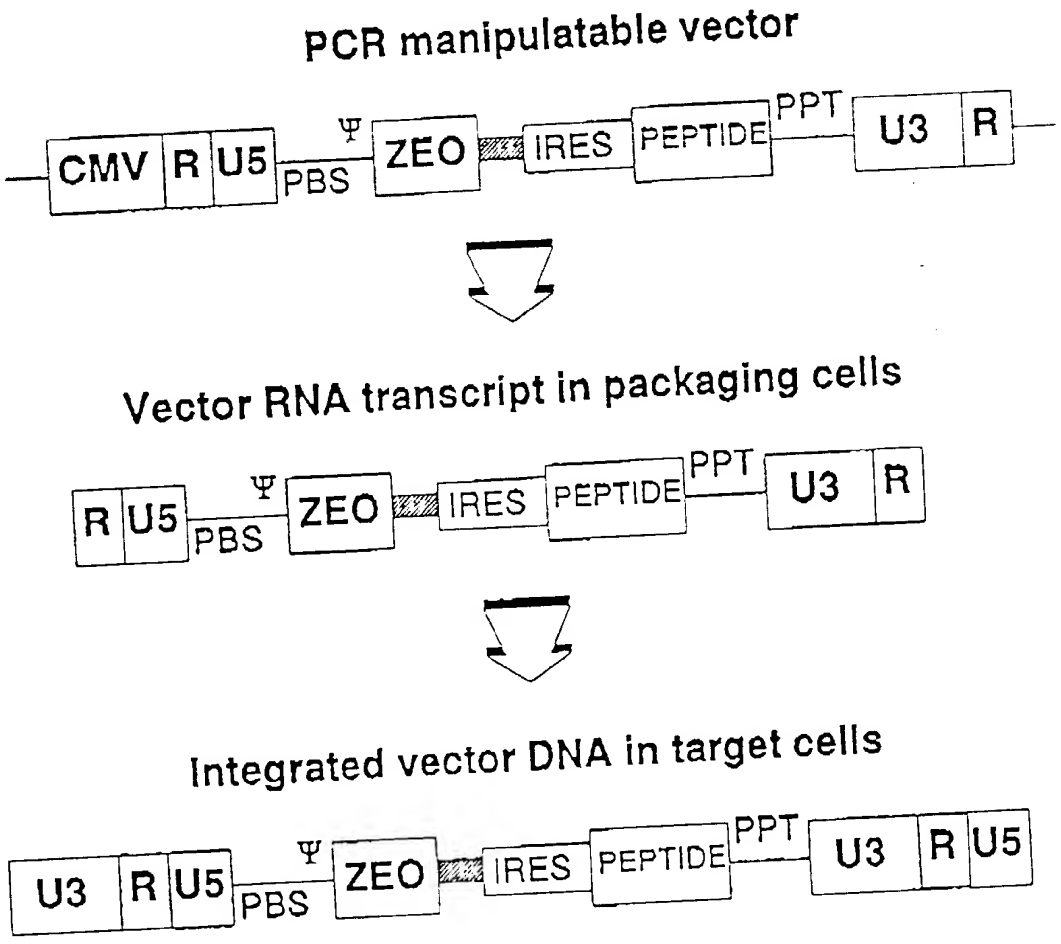
12. A method according to any one of claims 1-11 in which the random DNA sequences are introduced into, or fused to DNA sequences encoding larger proteins expressed simultaneously from the library vectors.

13. A method according to claim 12 in which the larger proteins are selected from secreted proteins, intracellular proteins, and membrane proteins e.g. signal transducing molecules.

14. A method according to any one of claims 1-13 which is used for identification of T cell epitopes.

15. A method according to any one of claims 1-13 which is used for identifying biologically active peptides which regulate cell surface expression of proteins.

Figure 1


PCR manipulatable vector
CMV
R
U5
PBS
Ψ
ZEO
IRES
PEPTIDE
PPT
U3
R
Vector RNA transcript in packaging cells
R
U5
PBS
Ψ
ZEO
IRES
PEPTIDE
PPT
U3
R
Integrated vector DNA in target cells
U3
R
U5
PBS
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ZEO
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